AMENDMENTS TO THE SPECIFICATION

In the Specification:

Please amend the specification as follows.

Please amend the title to read:

~~NOVEL~~ B7-4 POLYPEPTIDES ~~MOLECULES~~ AND USES THEREFOR

Please replace the paragraph on page 1, lines 5-6 with the following rewritten paragraph:

This application is a divisional application of U.S. application serial number 09/644,934, filed August 23, 2000, pending. This application [,] ~~which~~ claims priority to U.S. provisional application serial number 60/150,390, filed on August 23, 1999, which is ~~both of which are~~ incorporated herein in its ~~their~~ entirety by this reference.

Please replace the paragraph on page 10, lines 13-17 with the following rewritten paragraph:

The B7-4 molecules described herein are members of the B7 family of molecules. The term "B7 family" or "B7 molecules" as used herein includes costimulatory molecules that share sequence homology with B7 polypeptides, e.g., with B7-1, B7-2, B7-3 (recognized by the antibody BB-1), and/or B7-4. For example, human B7-1 and B7-2 share approximately 26% amino acid sequence identity when compared using the BLAST program at NCBI with the default parameters (Blosum62 matrix with gap penalties set at existence 11 and extension 1 (See the NCBI website ~~http://www.ncbi.nlm.nih.gov~~)).

Please replace the paragraphs on page 31, line 14 through page 32, line 9 with the following rewritten paragraph:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the GAP program in the GCG software package (available at the Genetics Computer Group website ~~http://www.gcg.com~~), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at the Genetics Computer Group website ~~http://www.gcg.com~~), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other

family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to B7-4 or PD-1 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to B7-4 or PD-1 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. For example, the nucleotide sequences of the invention were analyzed using the default Blastn matrix 1-3 with gap penalties set at: existence 11 and extension 1. The amino acid sequences of the invention were analyzed using the default settings: the Blosum 62 matrix with gap penalties set at existence 11 and extension 1. See the NCBI website ~~http://www.ncbi.nlm.nih.gov~~.

Please replace the paragraph on page 74, lines 4-14 with the following rewritten paragraph:

The cell-free assays of the present invention are amenable to use of both soluble and/or membrane-bound forms of proteins (e.g., B7-4 proteins or biologically active portions thereof, or receptors to which B7-4 binds). In the case of cell-free assays in which a membrane-bound form a protein is used (e.g., a cell surface B7-4 receptor) it may be desirable to utilize a solubilizing agent such that the membrane-bound form of the protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, ~~Triton~~ TRITON® X-100, ~~Triton~~ TRITON® X-114, ~~Thesit~~ THESIT®, Isotridecypoly(ethylene glycol ether)$_n$, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl=N,N-dimethyl-3-ammonio-1-propane sulfonate.

Please replace the paragraph on page 97, line 21 through page 98, line 2 with the following rewritten paragraph:

Sequencing revealed two forms of B7-4 molecules. The first form, B7-4 secreted (B7-4S) encodes a protein having a short hydrophilic domain without a membrane anchor. The nucleotide and amino acid sequences of this form are shown in SEQ ID NO:1 and 2, respectively. The second form, B7-4 membrane (B7-4M) encodes a protein having a transmembrane and short cytoplasmic domain. The nucleotide and amino acid sequences of this form are shown in SEQ ID NO:3 and 4, respectively. Both members of the B7-4 family identified have signal, IgV, and IgC domains, as illustrated in Figures 3 and 4. The B7-4M form has approximately 21% amino acid identity to human B7-1 and about 20% amino acid identity to human B7-2 as calculated using the default Blosum62 matrix with gap penalties set at existence 11 and extension 1 (See the NCBI website ~~http://www.ncbi.nlm.nih.gov~~), under conditions where B7-1 and B7-2 have about 26% identity.